STIC Biotechnology Systems Branch

RAW SEQUENCE LISTING
ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: _10/511,415A_
Source: _PCT/10_
Date Processed by STIC: _11/21/05_

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY
FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO **REDUCE** ERRORED SEQUENCE LISTINGS, PLEASE USE THE **CHECKER VERSION 4.2.2 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:
http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.
Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.
Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (**<http://www.uspto.gov/ebc/efs/downloads/documents.htm>** , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 01/14/05): U.S. Patent and Trademark Office, Mail Stop Sequence, Customer Window, Randolph Building, 401 Dulany Street, Alexandria, VA 22314

Revised 01/24/05

Raw Sequence Listing Error Summary

ERROR DETECTED	SUGGESTED CORRECTION	SERIAL NUMBER: /0/5//,4/5A

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1 _____ Wrapped Nucleics
Wrapped Aminos

The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."

2 _____ Invalid Line Length

The rules require that a line not exceed 72 characters in length. This includes white spaces.

3 _____ Misaligned Amino
Numbering

The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers: use space characters, instead.

4 _____ Non-ASCII

The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.

5 _____ Variable Length

Sequence(s)_____ contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.

6 _____ PatentIn 2.0
"bug"

A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.

7 _____ Skipped Sequences
(OLD RULES)

Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i)   SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.

8 _____ Skipped Sequences
(NEW RULES)

Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence.
<210> sequence id number
<400> sequence id number
000

9 _____ Use of n's or Xaa's
(NEW RULES)

Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

10 _____ Invalid <213>
Response

Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence

11 _____ Use of <220>

Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)

12 _____ PatentIn 2.0
"bug"

Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

13 _____ Misuse of n/Xaa

"n" can only represent a single <u>nucleotide</u>; "Xaa" can only represent a single <u>amino acid</u>

PCT

```
 3 <110> APPLICANT: Imperial College Innovations Limited
 5 <120> TITLE OF INVENTION: Methods
 7 <130> FILE REFERENCE: ICOY/P28304PC
 9 <140> CURRENT APPLICATION NUMBER: US/10/511,415A
10 <141> CURRENT FILING DATE: 2004-10-14
12 <150> PRIOR APPLICATION NUMBER: PCT/GB03/01625
13 <151> PRIOR FILING DATE: 2003-04-15
15 <160> NUMBER OF SEQ ID NOS: 30
17 <170> SOFTWARE: PatentIn version 3.1
19 <210> SEQ ID NO: 1
20 <211> LENGTH: 400
21 <212> TYPE: PRT
22 <213> ORGANISM: Homo sapiens
24 <400> SEQUENCE: 1
26 Met Met Asp Leu Arg Asn Thr Pro Ala Lys Ser Leu Asp Lys Phe Ile
27 1               5                   10                  15
30 Glu Asp Tyr Leu Leu Pro Asp Thr Cys Phe Arg Met Gln Ile Asp His
31             20                  25                  30
34 Ala Ile Asp Ile Ile Cys Gly Phe Leu Lys Glu Arg Cys Phe Arg Gly
35         35                  40                  45
38 Ser Ser Tyr Pro Val Cys Val Ser Lys Val Val Lys Gly Gly Ser Ser
39     50                  55                  60
42 Gly Lys Gly Thr Thr Leu Arg Gly Arg Ser Asp Ala Asp Leu Val Val
43 65                  70                  75                  80
46 Phe Leu Ser Pro Leu Thr Thr Phe Gln Asp Gln Leu Asn Arg Arg Gly
47             85                  90                  95
50 Glu Phe Ile Gln Glu Ile Arg Arg Gln Leu Glu Ala Cys Gln Arg Glu
51             100                 105                 110
54 Arg Ala Leu Ser Val Lys Phe Glu Val Gln Ala Pro Arg Trp Gly Asn
55             115                 120                 125
58 Pro Arg Ala Leu Ser Phe Val Leu Ser Ser Leu Gln Leu Gly Glu Gly
59         130                 135                 140
62 Val Glu Phe Asp Val Leu Pro Ala Phe Asp Ala Leu Gly Gln Leu Thr
63 145                 150                 155                 160
66 Gly Ser Tyr Lys Pro Asn Pro Gln Ile Tyr Val Lys Leu Ile Glu Glu
67             165                 170                 175
70 Cys Thr Asp Leu Gln Lys Glu Gly Glu Phe Ser Thr Cys Phe Thr Glu
71             180                 185                 190
74 Leu Gln Arg Asp Phe Leu Lys Gln Arg Pro Thr Lys Leu Lys Ser Leu
75         195                 200                 205
78 Ile Arg Leu Val Lys His Trp Tyr Gln Asn Cys Lys Lys Lys Leu Gly
79     210                 215                 220
82 Lys Leu Pro Pro Gln Tyr Ala Leu Glu Leu Leu Thr Val Tyr Ala Trp
```

RAW SEQUENCE LISTING   DATE: 11/21/2005
PATENT APPLICATION: US/10/511,415A   TIME: 15:45:49

Input Set : E:\20040873-seq5.List.txt
Output Set: N:\CRF4\11212005\J511415A.raw

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 83 225                  230             235                  240
 86 Glu Arg Gly Ser Met Lys Thr His Phe Asn Thr Ala Gln Gly Phe Arg
 87              245              250                  255
 90 Thr Val Leu Glu Leu Val Ile Asn Tyr Gln Gln Leu Cys Ile Tyr Trp
 91              260              265                  270
 94 Thr Lys Tyr Tyr Asp Phe Lys Asn Pro Ile Ile Glu Lys Tyr Leu Arg
 95          275              280                  285
 98 Arg Gln Leu Thr Lys Pro Arg Pro Val Ile Leu Asp Pro Ala Asp Pro
 99      290              295                  300
102 Thr Gly Asn Leu Gly Gly Gly Asp Pro Lys Gly Trp Arg Gln Leu Ala
103 305              310              315                  320
106 Gln Glu Ala Glu Ala Trp Leu Asn Tyr Pro Cys Phe Lys Asn Trp Asp
107              325              330                  335
110 Gly Ser Pro Val Ser Ser Trp Ile Leu Leu Ala Glu Ser Asn Ser Thr
111              340              345                  350
114 Asp Asp Glu Thr Asp Asp Pro Arg Thr Tyr Gln Lys Tyr Gly Tyr Ile
115          355              360                  365
118 Gly Thr His Glu Tyr Pro His Phe Ser His Arg Pro Ser Thr Leu Gln
119      370              375                  380
122 Ala Ala Ser Thr Pro Gln Ala Glu Glu Asp Trp Thr Cys Thr Ile Leu
123 385              390              395                  400
126 <210> SEQ ID NO: 2
127 <211> LENGTH: 1590
128 <212> TYPE: DNA
129 <213> ORGANISM: Homo sapiens
131 <400> SEQUENCE: 2
132 gaggcagttc tgttgccact ctctctcctg tcaatgatgg atctcagaaa taccccagcc      60
134 aaatctctgg acaagttcat tgaagactat ctcttgccag acacgtgttt ccgcatgcaa     120
136 atcgaccatg ccattgacat catctgtggg ttcctgaagg aaaggtgctt ccgaggtagc     180
138 tcctaccctg tgtgtgtgtc caaggtggta aagggtggct cctcaggcaa gggcaccacc     240
140 ctcagaggcc gatctgacgc tgacctggtt gtcttcctca gtcctctcac cactttcag     300
142 gatcagttaa atcgccgggg agagttcatc caggaaatta ggagacagct ggaagcctgt     360
144 caaagagaga gagcactttc cgtgaagttt gaggtccagg ctccacgctg gggcaacccc     420
146 cgtgcgctca gcttcgtact gagttcgctc cagctcgggg aggggtgga gttcgatgtg     480
148 ctgcctgcct ttgatgccct gggtcagttg actggcagct ataaacctaa cccccaaatc     540
150 tatgtcaagc tcatcgagga gtgcaccgac ctgcagaaag agggcgagtt ctccacctgc     600
152 ttcacagaac tacagagaga cttcctgaag cagcgcccca ccaagctcaa gagcctcatc     660
154 cgcctagtca agcactggta ccaaaattgt aagaagaagc ttgggaagct gccacctcag     720
156 tatgccctgg agctcctgac ggtctatgct tgggagcgag ggagcatgaa aacacatttc     780
158 aacacagccc aaggatttcg gacggtcttg gaattagtca taaactacca gcaactctgc     840
160 atctactgga caaagtatta tgactttaaa aaccccatta ttgaaaagta cctgagaagg     900
162 cagctcacga aacccaggcc tgtgatcctg gacccggcgg accctacagg aaacttgggt     960
164 ggtggagacc caaagggttg gaggcagctg gcacaagagg ctgaggcctg gctgaattac    1020
166 ccatgcttta agaattggga tgggtcccca gtgagctcct ggattctgct ggctgaaagc    1080
168 aacagtacag acgatgagac cgacgatccc aggacgtatc agaaatatgg ttacattgga    1140
170 acacatgagt accctcattt ctctcataga cccagcacgc tccaggcagc atccacccca    1200
172 caggcagaag aggactggac ctgcaccatc ctctgaatgc cagtgcatct gggggaaag    1260
174 ggctccagtg ttatctggac cagttccttc attttcaggt gggactcttg atccagagaa    1320
176 gacaaagctc ctcagtgagc tggtgtataa tccaagacag aacccaagtc tcctgactcc    1380
```

RAW SEQUENCE LISTING   DATE: 11/21/2005
PATENT APPLICATION: US/10/511,415A   TIME: 15:45:49

Input Set : E:\20040873-seq5.List.txt
Output Set: N:\CRF4\11212005\J511415A.raw

```
178 tggccttcta tgccctctat cctatcatag ataacattct ccacagcctc acttcattcc      1440
180 acctattctc tgaaaatatt ccctgagaga gaacagagag atttagataa gagaatgaaa      1500
182 ttccagcctt gactttcttc tgtgcacctg atgggagggt aatgtctaat gtattatcaa      1560
184 taacaataaa aataaagcaa ataccaaaaa                                       1590
187 <210> SEQ ID NO: 3
188 <211> LENGTH: 20
189 <212> TYPE: DNA
190 <213> ORGANISM: PCR primer
192 <400> SEQUENCE: 3
193 ctcactgagg agctttgtct                                                    20
196 <210> SEQ ID NO: 4
197 <211> LENGTH: 18
198 <212> TYPE: DNA
199 <213> ORGANISM: PCR primer
201 <400> SEQUENCE: 4
202 cactgaggag ctttgtcc                                                     18
205 <210> SEQ ID NO: 5
206 <211> LENGTH: 21
207 <212> TYPE: DNA
208 <213> ORGANISM: PCR primer
210 <400> SEQUENCE: 5
211 caggtgggac tcttgatcca g                                                 21
214 <210> SEQ ID NO: 6
215 <211> LENGTH: 20
216 <212> TYPE: DNA
217 <213> ORGANISM: PCR primer
219 <400> SEQUENCE: 6
220 agggttcctg gccgtgcagg                                                   20
223 <210> SEQ ID NO: 7
224 <211> LENGTH: 18
225 <212> TYPE: DNA
226 <213> ORGANISM: PCR primer
228 <400> SEQUENCE: 7
229 ccgcgctccc tcggctgc                                                     18
232 <210> SEQ ID NO: 8
233 <211> LENGTH: 20
234 <212> TYPE: DNA
235 <213> ORGANISM: PCR primer
237 <400> SEQUENCE: 8
238 atattctctt tgtaatcagg                                                   20
241 <210> SEQ ID NO: 9
242 <211> LENGTH: 20
243 <212> TYPE: DNA
244 <213> ORGANISM: PCR primer
246 <400> SEQUENCE: 9
247 aaaaatggca atcactcacc                                                   20
250 <210> SEQ ID NO: 10
251 <211> LENGTH: 20
252 <212> TYPE: DNA
```

(handwritten annotation) Invalid <213> response. See item 10 on Error Summary Sheet.

(handwritten annotation) This would be a sufficient explanation for <213 Artificial Sequence

```
253 <213> ORGANISM( PCR primer )
255 <400> SEQUENCE: 10
256 ccttctatga tttctcctag                                    20
259 <210> SEQ ID NO: 11
260 <211> LENGTH: 20
261 <212> TYPE: DNA
262 <213> ORGANISM( PCR primer )
264 <400> SEQUENCE: 11
265 atccaaaggc aatacgtacc                                    20
268 <210> SEQ ID NO: 12
269 <211> LENGTH: 20
270 <212> TYPE: DNA
271 <213> ORGANISM( PCR primer )
273 <400> SEQUENCE: 12
274 acagtgtttt atctttaagg                                    20
277 <210> SEQ ID NO: 13
278 <211> LENGTH: 21
279 <212> TYPE: DNA
280 <213> ORGANISM: PCR primer
282 <400> SEQUENCE: 13
283 gtaacattta ctacttactc g                                  21
286 <210> SEQ ID NO: 14
287 <211> LENGTH: 20
288 <212> TYPE: DNA
289 <213> ORGANISM: PCR primer
291 <400> SEQUENCE: 14
292 ccctgttcct tttaactagg                                    20
295 <210> SEQ ID NO: 15
296 <211> LENGTH: 20
297 <212> TYPE: DNA
298 <213> ORGANISM: PCR primer
300 <400> SEQUENCE: 15
301 ctcaggatca taatcactgc                                    20
304 <210> SEQ ID NO: 16
305 <211> LENGTH: 20
306 <212> TYPE: DNA
307 <213> ORGANISM: PCR primer
309 <400> SEQUENCE: 16
310 ctgtgaattt tatacccagg                                    20
313 <210> SEQ ID NO: 17
314 <211> LENGTH: 21
315 <212> TYPE: DNA
316 <213> ORGANISM: PCR primer
318 <400> SEQUENCE: 17
319 gtattacttt ttccacttac c                                  21
322 <210> SEQ ID NO: 18
323 <211> LENGTH: 20
324 <212> TYPE: DNA
325 <213> ORGANISM( PCR primer )
```

```
327 <400> SEQUENCE: 18
328 gactctcact gtcattgcag                                              20
331 <210> SEQ ID NO: 19
332 <211> LENGTH: 20
333 <212> TYPE: DNA
334 <213> ORGANISM: PCR primer
336 <400> SEQUENCE: 19
337 gtgtcattgc actccagcct                                              20
340 <210> SEQ ID NO: 20
341 <211> LENGTH: 624
342 <212> TYPE: DNA
343 <213> ORGANISM: Homo sapiens
345 <400> SEQUENCE: 20
346 ggatccagat ggcatgtcac agtatactaa atgctcactg aatccagctg caatgcagga   60
348 agactcccct gatgtgatca tgtgtctcac cctttcaggc tgaaagcaac agtacagacg  120
350 atgagaccga cgatcccagg acgtatcaga aatatggtta cattggaaca catgagtacc  180
352 ctcatttctc tcatagaccc agcacgctcc aggcagcatc caccccacag gcagaagagg  240
354 actggacctg caccatcctc tgaatgccag tgcatcttgg gggaaagggc tccagtgtta  300
356 tctggaccag ttccttcatt ttcaggtggg actcttgatc cagagaagac aaagctcctc  360
358 agtgagctgg tgtataatcc aagacagaac ccaagtctcc tgactcctgg ccttctatgc  420
360 cctctatcct atcatagata acattctcca cagcctcact tcattccacc tattctctga  480
362 aaatattccc tgagagagaa cagagagatt tagataagag aatgaaattc cagccttgac  540
364 tttcttctgt gcacctgatg ggagggtaat gtctaatgta ttatcaataa caataaaaat  600
366 aaagcaaata ccatttattg ggtg                                         624
369 <210> SEQ ID NO: 21
370 <211> LENGTH: 19
371 <212> TYPE: DNA
372 <213> ORGANISM: PCR primer
374 <400> SEQUENCE: 21
375 ggcctggcct gacaactat                                               19
378 <210> SEQ ID NO: 22
379 <211> LENGTH: 19
380 <212> TYPE: DNA
381 <213> ORGANISM: PCR primer
383 <400> SEQUENCE: 22
384 catccaagcc tgcacgtat                                               19
387 <210> SEQ ID NO: 23
388 <211> LENGTH: 20
389 <212> TYPE: DNA
390 <213> ORGANISM: PCR primer
392 <400> SEQUENCE: 23
393 gctttgtgtg agcaacatgg                                              20
396 <210> SEQ ID NO: 24
397 <211> LENGTH: 20
398 <212> TYPE: DNA
399 <213> ORGANISM: PCR primer
401 <400> SEQUENCE: 24
402 ggctcatctg gtctctccag                                              20
405 <210> SEQ ID NO: 25
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Please correct this error in subsequent sequences

VERIFICATION SUMMARY   DATE: 11/21/2005
PATENT APPLICATION: **US/10/511,415A**   TIME: 15:45:50

Input Set : **E:\20040873-seq5.List.txt**
Output Set: **N:\CRF4\11212005\J511415A.raw**